```
           CCCTGTCAGTCTTAAGATTCTAGAAGTCGCTGTCCTATACGGAACCCAAAA
    CTCTCACTGTTAATGAAATACCATTGTCGGGGCGAAGATGTAGCTCAGTGGTAAAATACT -121

    TGCCAGCACACACAAGAATTAGACTTCAACCGTCACCAACTGCCCTGTGTAGGACGGTCG
    GTCACTGAAAGAGAATATTGTCTGCAATACTCTAATGACATCTGTCTGTGTTCATCTGAA -1

                                              SP
  1 MetPheHisLeuLysHisSerSerLeuThrValGlyProPheIleSerValMetIleLeu
    ATGTTCCATTTAAAACACAGCAGCCTTACTGTTGGACCATTTATCTCAGTAATGATTCTG

    LeuArgPheLeuCysThrGlyArgAsnAsnSerLysGlyArgSerLeuIleGlyArgLeu
    CTCCGCTTTCTTTGTACAGGACGCAACAACAGTAAAGGAAGAAGTCTTATTGGCAGATTA 120

 41 GluThrGlnProProIleThrGlyLysGlyValProValGluProGlyPheSerIleAsp
    GAAACCCAGCCTCCAATCACTGGGAAAGGGGTTCCGGTAGAACCAGGCTTTTCCATCGAT

    GluPheSerAlaSerIleLeuThrGlyLysLeuThrThrValPheLeuProValValTyr
    GAGTTCTCTGCGTCCATCCTCACCGGGAAGCTGACCACGGTCTTTCTTCCGGTCGTCTAC 240

                                   I
 81 IleIleValPheValIleGlyLeuProSerAsnGlyMetAlaLeuTrpIlePheLeuPhe
    ATTATTGTGTTTGTGATTGGTTTGCCCAGTAATGGCATGGCCCTCTGGATCTTCCTTTTC

                                               II
    ArgThrLysLysLysHisProAlaValIleTyrMetAlaAsnLeuAlaLeuAlaAspLeu
    CGAACGAAGAAGAAACACCCCGCCGTGATTTACATGGCCAACCTGGCCTTGGCCGACCTC 360

121 LeuSerValIleTrpPheProLeuLysIleSerTyrHisLeuHisGlyAsnAsnTrpVal
    CTCTCTGTCATCTGGTTCCCCCTGAAGATCTCCTACCACCTACATGGCAACAACTGGGTC

                                               III
    TyrGlyGluAlaLeuCysLysValLeuIleGlyPhePheTyrGlyAsnMetTyrCysSer
    TACGGGGAGGCCCTGTGCAAGGTGCTCATTGGCTTTTTCTATGGTAACATGTATTGCTCC 480

161 IleLeuPheMetThrCysLeuSerValGlnArgTyrTrpValIleValAsnProMetGly
    ATCCTCTTCATGACCTGCCTCAGCGTGCAGAGGTACTGGGTGATCGTGAACCCCATGGGA

                                               IV
    HisProArgLysLysAlaAsnIleAlaValGlyValSerLeuAlaIleTrpLeuLeuIle
    CACCCCAGGAAGAAGGCAAACATCGCCGTTGGCGTCTCCTTGGCAATCTGGCTCCTGATT 600
```

FIG.1A

```
201 PheLeuValThrIleProLeuTyrValMetLysGlnThrIleTyrIleProAlaLeuAsn
    TTTCTGGTCACCATCCCTTTGTATGTCATGAAGCAGACCATCTACATTCCAGCATTGAAC

    IleThrThrCysHisAspValLeuProGluGluValLeuValGlyAsnMetPheAsnTyr
    ATCACCACCTGTCACGATGTGCTGCCTGAGGAGGTATTGGTGGGGGACATGTTCAATTAC 720

                               V
241 PheLeuSerLeuAlaIleGlyValPheLeuPheProAlaLeuLeuThrAlaSerAlaTyr
    TTCCTCTCACTGGCCATTGGAGTCTTCCTGTTCCCGGCCCTCCTTACTGCATCTGCCTAC

    ValLeuMetIleLysThrLeuArgSerSerAlaMetAspGluHisSerGluLysLysArg
    GTGCTCATGATCAAGACGCTCCGCTCTTCTGCTATGGATGAACACTCAGAGAACAAAAGG 840

                                         VI
281 GlnArgAlaIleArgLeuIleIleThrValLeuAlaMetTyrPheIleCysPheAlaPro
    CAGAGGGCTATCCGACTCATCATCACCGTGCTGGCCATGTACTTCATCTGCTTTCGTCCT

    SerAsnLeuLeuLeuValValHisTyrPheLeuIleLysThrGlnArgGlnSerHisVal
    AGCAACCTTCTGCTCGTAGTGCATTATTTCCTAATCAAAACCCAGAGGCAGAGCCACGTC 960

                                        VII
321 TyrAlaLeuTyrLeuValAlaLeuCysLeuSerThrLeuAsnSerCysIleAspProPhe
    TACGCCCTCTACCTTGTCGCCCTCTGCCTGTCGACCCTCAACAGCTGCATAGACCCCTTT

    ValTyrTyrPheValSerLysAspPheArgAspHisAlaArgAsnAlaLeuLeuCysArg
    GTCTATTACTTTGTCTCAAAAGATTTCAGGGATCACGCCAGAAACGCGCTCCTCTGCCGA 1080

361 SerValArgThrValAsnArgMetGlnIleSerLeuSerSerAsnLysPheSerArgLys
    AGTGTCCGCACTGTGAATCGCATGCAAATCTCGCTCAGCTCCAACAAGTTCTCCAGGAAG
    GATGTCAAGCCTGCTTGATGATGATGATGATGATGGTGTGTGTGTG              1246

    SerGlySerTyrSerSerSerSerThrSerValLysThrSerTyr
    TCCGGCTCCTACTCTTCAAGCTCAACCAGTGTTAAAACCTCCTACTGAGCTGTACCTGAG 1200
```

FIG. 1B

```
     CGCTCCAGGCCTGGGTGACAGCGAGACCCTGTCTCATAAATTAAAAAATGAATAA

                                     SP
MetAsnValLeuSerPheGluGlnThrSerValThrAlaGluThrPheIleSerValMet
ATGAATGTACTTTCATTTGAACAAACCAGTGTTACTGCTGAAACATTTATTTCTGTAATG

ThrLeuValPheLeuSerCysThrGlyThrAsnArgSerSerLysGlyArgSerLeuIle   -1
ACCCTTGTCTTCCTTTCTTGTACAGGAACCAATAGATCCTCTAAAGGAAGAAGCCTTATT  120

GlyLysValAspGlyThrSerHisValThrGlyLysGlyValThrValGluThrValPhe
GGTAAGGTTGATGGCACATCCCACGTCACTGGAAAAGGAGTTACAGTTGAAACAGTCTTT

SerValAspGluPheSerAlaSerValLeuThrGlyLysLeuThrThrValPheLeuPro
TCTGTGGATGAGTTTTCTGCATCTGTCCTCACTGGAAAACTGACCACTGTCTTCCTTCCA  240

                                    I
IleValTyrThrIleValPheValValGlyLeuProSerAsnGlyMetAlaLeuTrpVal
ATTGTCTACACAATTGTGTTTGTGGTGGGTTTGCCAAGTAACGGCATGGCCCTGTGGGTC

PheLeuPheArgThrLysLysLysHisProAlaValIleTyrMetAlaAsnLeuAlaLeu
TTTCTTTTCCGAACTAAGAAGAAGCACCCTGCTGTGATTTACATGGCCAATCTGGCCTTG  360

      II
AlaAspLeuLeuSerValIleTrpPheProLeuLysIleAlaTyrHisIleHisGlyAsn
GCTGACCTCCTCTCTGTCATCTGGTTCCCCTTGAAGATTGCCTATCACATACATGGCAAC

AsnTrpIleTyrGlyGluAlaLeuCysAsnValLeuIleGlyPhePheTyrGlyAsnMet
AACTGGATTTATGGGGAAGCTCTTTGTAATGTGCTTATTGGCTTTTTCTATGGCAACATG  480

      III
TyrCysSerIleLeuPheMetThrCysLeuSerValGlnArgTyrTrpValIleValAsn
TACTGTTCCATTCTCTTCATGACCTGCCTCAGTGTGCAGAGGTATTGGGTCATCGTGAAC

ProMetGlyHisSerArgLysLysAlaAsnIleAlaIleGlyIleSerLeuAlaIleTrp
CCCATGGGGCACTCCAGGAAGAAGGCAAACATTGCCATTGGCATCTCCCTGGCAATATGG  600
```

FIG.2A

```
         IV
LeuLeuIleLeuLeuValThrIleProLeuTyrValValLysGlnThrIlePheIlePro
CTGCTGATTCTGCTGGTCACCATCCCTTTGTATGTCGTGAAGCAGACCATCTTCATTCCT

AlaLeuAsnIleThrThrCysHisAspValLeuProGluGlnLeuLeuValGlyAspMet
GCCCTGAACATCACGACCTGTCATGATGTTTTGCCTGAGCAGCTCTTGGTGGGAGACATG   720

                                                   V
PheAsnTyrPheLeuSerLeuAlaIleGlyValPheLeuPheProAlaPheLeuThrAla
TTCAATTACTTCCTCTCTCTGGCCATTGGGGTCTTTCTGTTCCCAGCCTTCCTCACAGCC

SerAlaTyrValLeuMetIleArgMetLeuArgSerSerAlaMetAspGluAsnSerGlu
TCTGCCTATGTGCTGATGATCAGAATGCTGCGATCTTCTGCCATGGATGAAAACTCAGAG   840

                                                      VI
LysLysArgLysArgAlaIleLysLeuIleValThrValLeuAlaMetTyrLeuIleCys
AAGAAAAGGAAGAGGGCCATCAAACTCATTGTCACTGTCCTGGCCATGTACCTGATCTGC

PheThrProSerAsnLeuLeuLeuValValHisTyrPheLeuIleLysSerGlnGlyGln
TTCACTCCTAGTAACCTTCTGCTTGTGGTGCATTATTTTCTGATTAAGAGCCAGGGCCAG   960

                                                  VII
SerHisValTyrAlaLeuTyrIleValAlaLeuCysLeuSerThrLeuAsnSerCysIle
AGCCATGTCTATGCCCTGTACATTGTAGCCCTCTGCCTCTCTACCCTTAACAGCTGCATC

AspProPheValTyrTyrPheValSerHisAspPheArgAspHisAlaLysAsnAlaLeu
GACCCCTTTGTCTATTACTTTGTTTCACATGATTTCAGGGATCATGCAAAGAACGCTCTC  1080

LeuCysArgSerValArgThrValLysGlnMetGlnValSerLeuThrSerLysLysHis
CTTTGCCGAAGTGTCCGCACTGTAAAGCAGATGCAAGTATCCCTCACCTCAAAGAAACAC

SerArgLysSerSerSerTyrSerSerSerSerThrThrValLysThrSerTyr *
TCCAGGAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGTTAAGACCTCCTATTGAGTT  1200
```

FIG. 2B

```
Mouse C140 M--FHLKHSS LIVGPFISVM ILLRFLCTGR NNSHKGRSLI GRLETQPPIT  47
Human C140 MNVLSFEQTS VTAETFISVM ILVFLSCTGT NRSSKGRSLI GKVDGTSHVT  50

Mouse C140 GKGVFVEPGF SIDEFSASIL TCKLTTVFLP VVYIIVFVIG LPSNGMALWI  97
Human C140 GKGVIVEIVF SMDEFSASVL TGKLTTVFLP IVYIIVFVVG LPSNGMALWV 100

Mouse C140 FLFRTKKKHP AVIYMANLAL ADLLSVIWFP LKISYHLHGN NWVYGEALCK 147
Human C140 FLFRTKKKHP AVIYMANLAL ADLLSVIWFP LKIAYHIHGN NWIYGEALCN 150

Mouse C140 VLIGFFYGNM YCSILFMTCL SVQRYWVIVN PMGHPRKKAN IAVGVSLAIW 197
Human C140 VLIGFFYGNM YCSILFMTCL SVQRYWVIVN PMGHSRKKAN IAIGISLAIW 200

Mouse C140 LLIFLVTIPL YVMKQTIYIP ALNITTCHDV LPEEVLVGDM FNYFLSLAIG 247
Human C140 LLILLVTIPL YVVKQTIPIP ALNITTCHDV LPEQLLVGDM FNYFLSLAIG 250

Mouse C140 VFLFPALLTA SAYVLMIKTL RSSAMDEHSE KKRQRAIRLI ITVLAMYFIC 297
Human C140 VFLFPAFLTA SAYVLMIRML RSSAMDENSE KKRKRAIKLI VTVLAMYLIC 300

Mouse C140 FAPSNLLLVV HYFLIKIQRQ SHVYALYLVA LCLSTLNSCI DPFVYYFVSK 347
Human C140 FIPSNLLLVV HYFLIKSQGQ SHVYALYIVA LCLSTLNSCI DPFVYYFVSH 350

Mouse C140 DFRDHARNAL LCRSVRTVNR MQISLSSNKF SRKSGSYSSS STSVKTSY   395
Human C140 DFRDHAKNAL LCRSVRTVKQ MQMSLISKKH SRKSSSYSSS STTVKTSY   398
```

FIG.3

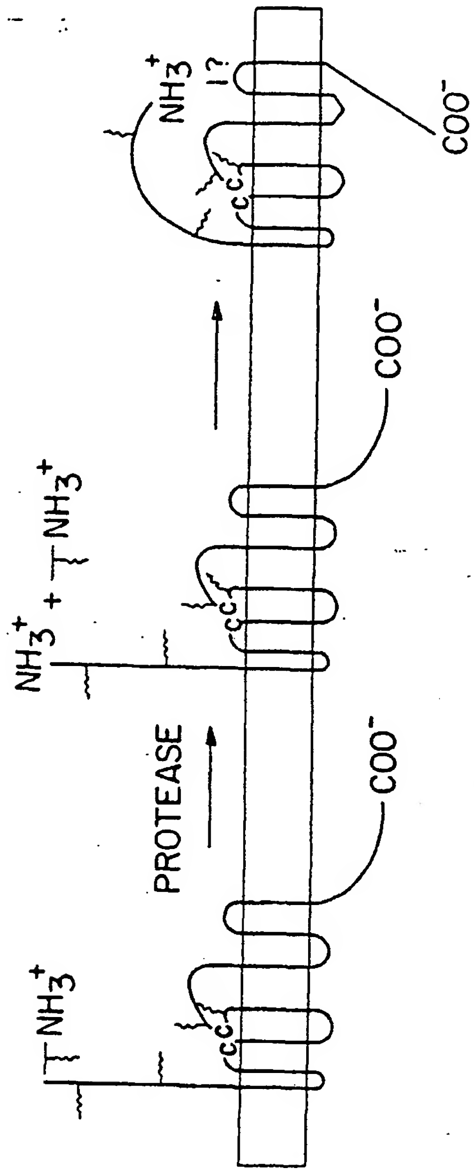

FIG.4

```
                 SP                            ▼
C140    MFHLKHSSLTVGPFISVMILLRFLCTGRNNSK-------GRSLIGRLETQP---------  44
HSTHRR  MGPRRLLLVAACFSLCGPLLSARTRARRPESKATNATLDPRSFLLRNPNDKYEPEWEDEE  60

                                                                I
C140    -------------PITGKGVPVEPGFSIDEFSASILTGKLTTVFLPVVYIIVFVIGLPSN  91
HSTHRR  KNESGLTEYRLVSINKSSPLQKQLPAFISEDASGYLTSSWLTLFVPSVYTGVFVVSLPLN 120

                                II
C140    GMALWIFLFRTKKKHPAVIYMANLALADLLSVIWFPLKISYHLHGNNWVYGEALCKVLIG 151
HSTHRR  IMAIVVFILKMKVKKPAVVYMLHLATADVLFVSVLPFKISYYFSGSDWQFGSELCRFVTA 180

           III                                       IV
C140    FFYGNMYCSILFMTCLSVQRYWVIVNPM-GHPRKKANIAVGVSLAIWLLIFLVTIPLYVM 210
HSTHRR  AFYCNMYASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAIWALAIAGVVPLVLK 240

                                                  V
C140    KQTIYIPALNITTCHDVLPEEVLVGDMFNYFLSLAIGVFLFPALLTASAYVLMIKTLRSS 270
HSTHRR  EQTIQVPGLNITTCHDVLNETLLEGYYAYYFSAFSAVFFFVPLIISTVCYVSIIRCLSSS 300

                            VI
C140    AMDEHSEKKRQRAIRLIITVLAMYFICFAPSNLLLVVHY-FLIKTQRQSHVYALYLVALC 329
HSTHRR  AVANRSKKSR--ALFLSAAVFCIFIICFGPTNVLLIAHYSFLSHTSTTEAAYFAYLLCVC 358

          VII
C140    LSTLNSCIDPFVYYFVSKDFRDHARNALLCRSVRTVNRMQISLSSNKFSRKSGSYSSSST 389
HSTHRR  VSSISSCIDPLIYYYASSECQRYVYSILCCKESSDPSSYNSSGQLMASKMDTCSSNLNNS 418

C140    SVKTSY-                                                      395
HSTHRR  IYKKLLT                                                      426
```

FIG.5

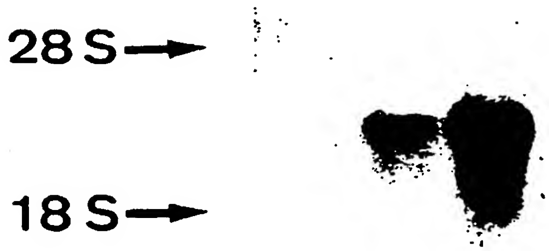

FIG. 6

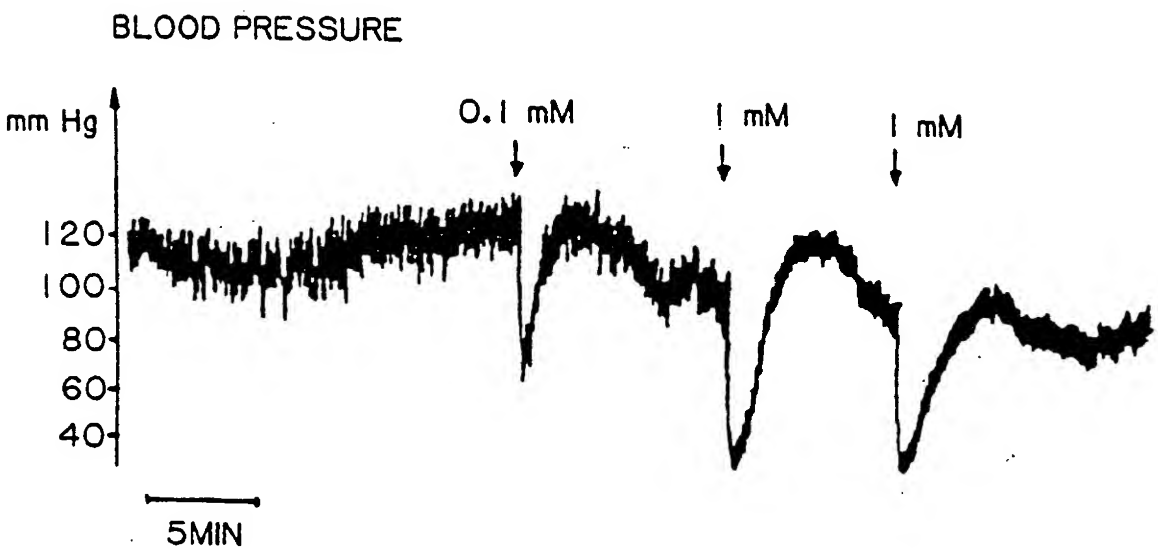

FIG. 7

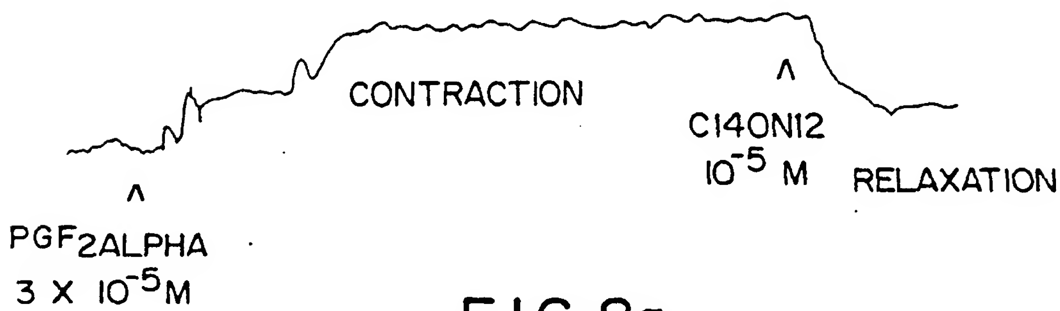
CONTRACTION
C140N12
10^{-5} M
RELAXATION
PGF2ALPHA
3×10^{-5} M

FIG. 8a

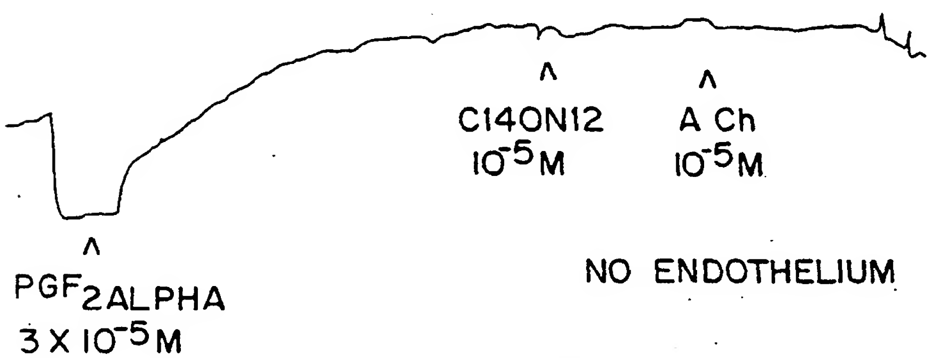
C140N12
10^{-5} M
A Ch
10^{-5} M
PGF2ALPHA
3×10^{-5} M
NO ENDOTHELIUM

FIG. 8b

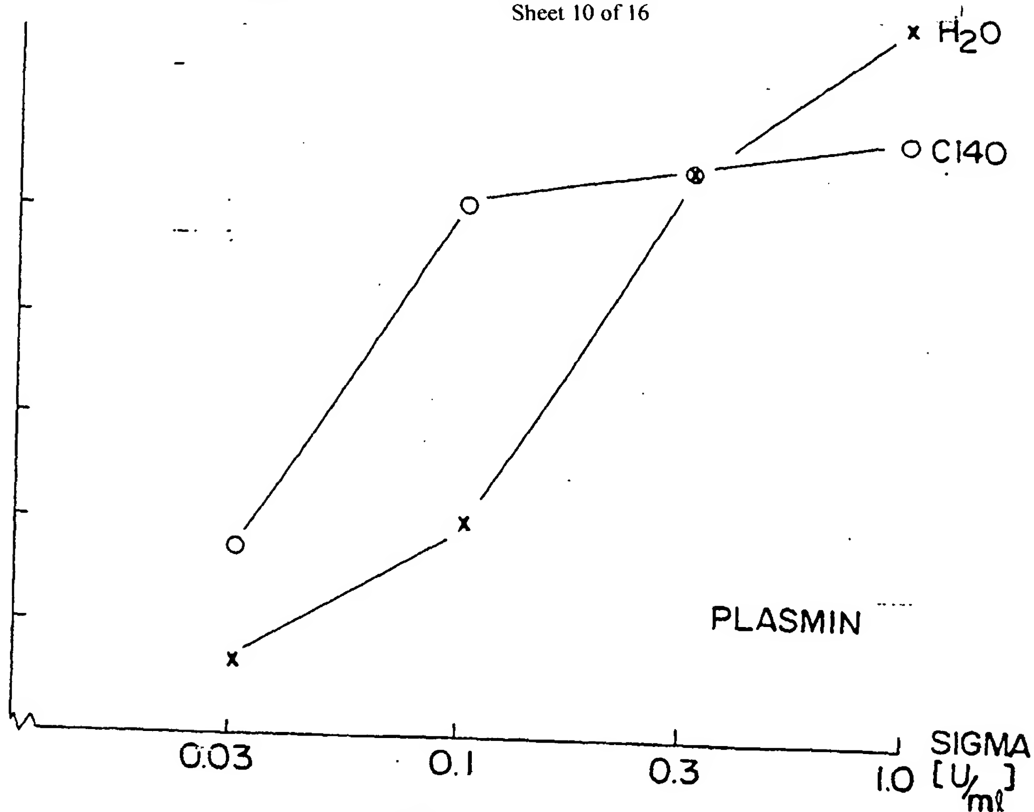
H_2O
C140
PLASMIN
0.03
0.1
0.3
1.0
SIGMA [U/ml]

FIG. 9a

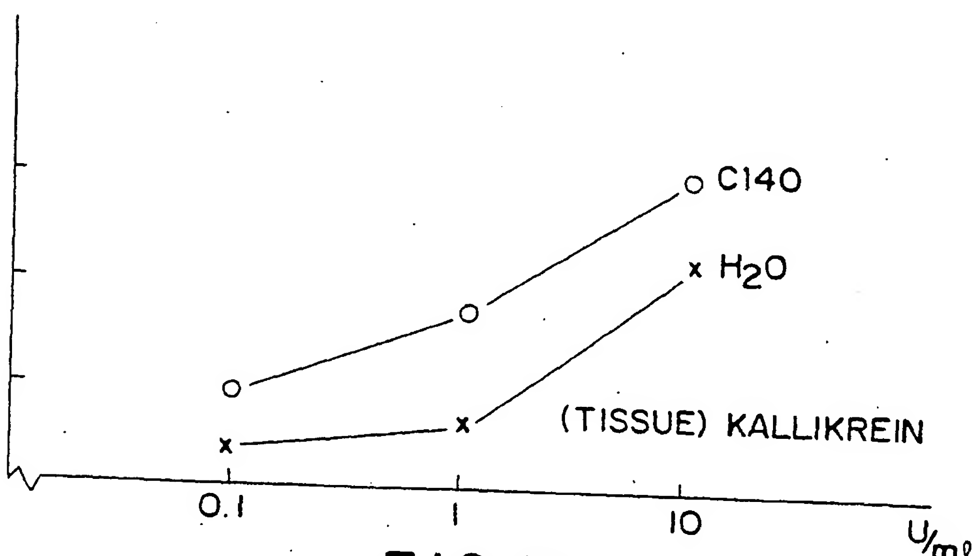
C140
H_2O
(TISSUE) KALLIKREIN
0.1
1
10
U/ml

FIG. 9b

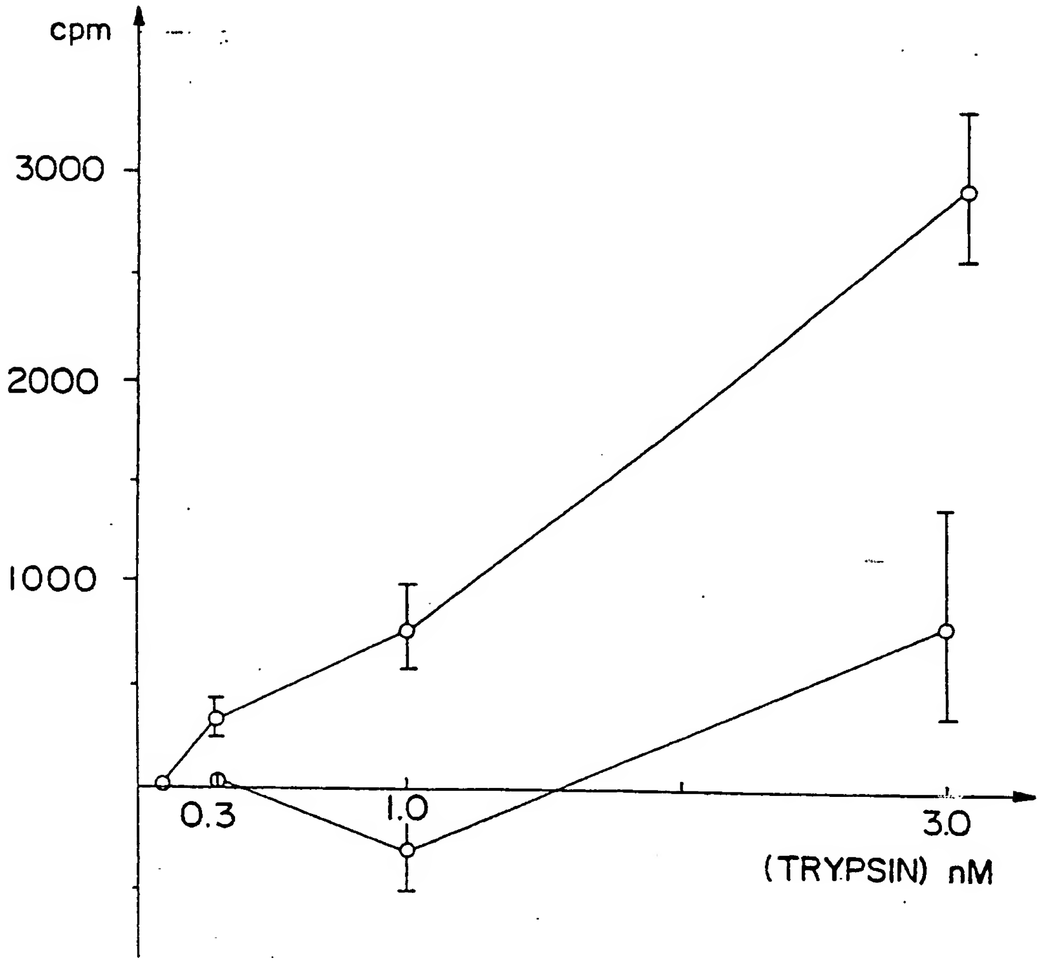

FIG.9c

```
CCCTGTGCTCAGAGTAGGGCTCCGAGTTTCGAACCACTGGTGGCGGATTGCCCGCCCGCC

CCACGTCCGGGGATGCGAAGTCTCAGCCTGGCGTGGCTGCTGGGAGGTATCACCCTTCTG
            M  R  S  L  S  L  A  W  L  L  G  G  I  T  L  L

GCGGCCTCGGTCTCCTGCAGCCGGACCGAGAACCTTGCACCGGGACGCAACAACAGTAAA
A  A  S  V  S  C  S  R  T  E  N  L  A  P  G  R  N  N  S  K

GGAAGAAGTCTTATTGGCAGATTAGAAACCCAGCCTCCAATCACTGGGAAAGGGGTTCCG
G  R  S  L  I  G  R  L  E  T  Q  P  P  I  T  G  K  G  V  P

GTAGAACCAGGCTTTTCCATCGATGAGTTCTCTGCGTCCATCCTCACCGGGAAGCTGACC
V  E  P  G  F  S  I  D  E  F  S  A  S  I  L  T  G  K  L  T

ACGGTCTTTCTTCCGGTCGTCTACATTATTGTGTTTGTGATTGGTTTGCCCAGTAATGGC
T  V  F  L  P  V  V  Y  I  I  V  F  V  I  G  L  P  S  N  G

ATGGCCCTCTGGATCTTCCTTTTCCGAACGAAGAAGAAACACCCCGCCGTGATTTACATG
M  A  L  W  I  F  L  F  R  T  K  K  K  H  P  A  V  I  Y  M

GCCAACCTGGCCTTGGCCGACCTCCTCTCTGTCATCTGGTTCCCCCTGAAGATCTCCTAC
A  N  L  A  L  A  D  L  L  S  V  I  W  F  P  L  K  I  S  Y

CACCTACATGGCAACAACTGGGTCTACGGGGAGGCCCTGTGCAAGGTGCTCATTGGCTTT
H  L  H  G  N  N  W  V  Y  G  E  A  L  C  K  V  L  I  G  F

TTCTATGGTAACATGTATTGCTCCATCCTCTTCATGACCTGCCTCAGCGTGCAGAGGTAC
F  Y  G  N  M  Y  C  S  I  L  F  M  T  C  L  S  V  Q  R  Y

TGGGTGATCGTGAACCCCATGGGACACCCCAGGAAGAAGGCAAACATCGCCGTTGGCGTC
W  V  I  V  N  P  M  G  H  P  R  K  K  A  N  I  A  V  G  V

TCCTTGGCAATCTGGCTCCTGATTTTTCTGGTCACCATCCCTTTGTATGTCATGAAGCAG
S  L  A  I  W  L  L  I  F  L  V  T  P  I  L  Y  V  M  K  Q

ACCATCTACATTCCAGCATTGAACATCACCACCTGTCACGATGTGCTGCCTGAGGAGGTA
T  I  Y  I  P  A  L  N  I  T  T  C  H  D  V  L  P  E  E  V

TTGGTGGGGGACATGTTCAATTACTTCCTCTCACTGGCCATTGGAGTCTTCCTGTTCCCG
L  V  G  D  M  F  N  Y  F  L  S  L  A  I  G  V  F  L  F  P

GCCCTCCTTACTGCATCTGCCTACGTGCTCATGATCAAGACGCTCCGCTCTTCTGCTATG
A  L  L  T  A  S  A  Y  V  L  M  I  K  T  L  R  S  S  A  M

GATGAACACTCAGAGAAGAAAAGGCAGAGGGCTATCCGACTCATCATCACCGTGCTGGCC
D  E  H  S  E  K  K  R  Q  R  A  I  R  L  I  I  T  V  L  A

ATGTACTTCATCTGCTTTGCTCCTAGCAACCTTCTGCTCGTAGTGCATTATTTCCTAATC
M  Y  F  I  C  F  A  P  S  N  L  L  L  V  V  H  Y  F  L  I

AAAACCCAGAGGCAGAGCCACGTCTACGCCCTCTACCTTGTCGCCCTCTGCCTGTCGACC
K  T  Q  R  Q  S  H  V  Y  A  L  Y  L  V  A  L  C  L  S  T

CTCAACAGCTGCATAGACCCCTTTGTCTATTACTTTGTCTCAAAAGATTTCAGGGATCAC
L  N  S  C  I  D  P  F  V  Y  Y  F  V  S  K  D  F  R  D  H
```

FIG. 10A

```
GCCAGAAACGCGCTCCTCTGCCGAAGTGTCCGCACTGTGAATCGCATGCAAATCTCGCTC
A  R  N  A  L  L  C  R  S  V  R  T  V  N  R  M  Q  I  S  L

AGCTCCAACAAGTTCTCCAGGAAGTCCGGCTCCTACTCTTCAAGCTCAACCAGTGTTAAA
S  S  N  K  F  S  R  K  S  G  S  Y  S  S  S  S  T  S  V  K

ACCTCCTACTGAGCTGTACCTGAGGATGTCAAGCCTGCTTGATGATGATGATGATGATGG
T  S  Y

TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACCCGTGTGTGAGTGCGTG

GTAGGGATACACCAACATGGATGGGGCTGTCATTTCCTATCCAAGCTGTCTGTCTCTGCA

CCAATCACAAGCATGCAGCTCTCCCCAGGATTGACAGAAGCCTCCTCCTTTGCATGAGAA

CAGTCTTCCACTCTGATGAAAAGCATCAGTATCAGAAACTGAAACGAACTGAGAGGAGCT

TGTTTTGTGAAAGTGAAGAGAAGATGGAGGGTCAGTGACTTGCAAAAAAAACCAACCAAA

CAAAAACTACACCTGGCAAGAAGGCTAAGACTCTCTGAAATGCTTCCCTTTTCCATCTGG

AGTTCGTCTCGGCCTTGTTCAGGACCTGAGGCCCTGGTAGAGCTTCAGTCCAGTTGATTG

ACTTTACAGACTTGAGAGAGGAGTGAATGAGGAGTGAATGAGGCTCCTGGCGGCATCCTA

ACCGGCTAACAGTGGCCTTGCTGGACAATAGGATTCAGATGGCTGGAGTTACATTCTCAC

ACCATTTCATCAGAACTATTGGGGATCTTGATCAATGTGCAGGTCCCTTAGCGTCAGTAA

CCCTGGGAGCTCAGACACGATGGGGGTGAGGGTGGGGGTGGGGGTGGGGGTGAGGCTCTA

CAAACCTTAGTGATGACTGCAGACACAGAACCATGGAGCTGAGCCTGCTTCTGCTTGCCA

GGGCACCACTGTAATGTTGGCAAAGAAAAACCAACAGCAGTGTTTTGAGCCTCTTTTTTT

GGTCAGTTTATGATGAATTTGCCTATTGGTTTATTGGGATTTTCAGTTCCTTTATTACTT

TGTTGTAATTTTGTGTGTTTATTAGTCAAGAAAAAGAAGATGAGGCTCTTAAAAATGTAA

ATAAAATTTTTGGTTTTTTGGTTTTTTAACTTGGGCCAACTACAAATACTGCTTAGGTTT

TTTTCTAACTTAATTGTTAACTACATCATGTGAACTTAAGACATTTTCATGATAAAGCAT

TACTGTAGTGTCAGTTTTCCCTCATCCTCGATCATAGTCCTTCCCGTGAAGCAGGGCCCT

TCCCCTCCCCCCCCTTTGCCGTTTCCCTCCCCACCAGATAGTCCCCCTGTCTGCTTTAAC

CTACCAGTTAGTATTTTATAAAAACAGATCATTGGAATATTTATTATCAGTTTTGTTCAC

TTGTTATCAGTTTTGTTCACTAATTTGTCCAATAATGGAATTAACGTCTTCTCATCTGTT

TGAGGAAGATCTGAAACAAGGGGCCATTGCAGGAGTACATGGCTCCAGGCTTACTTTATA

TACTGCCTGTATTTGTGGCTTTAAAAAAATGACCTTGTTATATGAATGCTTTATAAATAA

ATAATGCATGAACTTTAAAAAAAAAAAAAAA
```

FIG. 10B

```
         10        20        30        40        50        60
123456789012345678901234567890123456789012345678901234567890
CAAAGAATTGTAATACGACTCACTATAGGGCGAATTCGGATCCAGGAGGATGCGGAGCCC
                                                MetArgSerPr

         70        80        90       100       110       120
123456789012345678901234567890123456789012345678901234567890
CAGCGCGGCGTGGCTGCTGGGGGCCGCCATCCTGCTAGCAGCCTCTCTCTCCTGCAGTGG     120
oSerAlaAlaTrpLeuLeuGlyAlaAlaIleLeuLeuAlaAlaSerLeuSerCysSerGl

CACCATCCAAGGAACCAATAGATCCTCTAAAGGAAGAAGCCTTATTGGTAAGGTTGATGG
yThrIleGlnGlyThrAsnArgSerSerLysGlyArgSerLeuIleGlyLysValAspGl

CACATCCCACGTCACTGGAAAAGGAGTTACAGTTGAAACAGTCTTTTCTGTGGATGAGTT     240
yThrSerHisValThrGlyLysGlyValThrValGluThrValPheSerValAspGluPh

TTCTGCATCTGTCCTCGCTGGAAAACTGACCACTGTCTTCCTTCCAATTGTCTACACAAT
eSerAlaSerValLeuAlaGlyLysLeuThrThrValPheLeuProIleValTyrThrIl

TGTGTTTGCGGTGGGTTTGCCAAGTAACGGCATGGCCCTATGGGTCTTTCTTTTCCGAAC     360
eValPheAlaValGlyLeuProSerAsnGlyMetAlaLeuTrpValPheLeuPheArgTh

TAAGAAGAAGCACCCTGCTGTGATTTACATGGCCAATCTGGCCTTGGCTGACCTCCTCTC
rLysLysLysHisProAlaValIleTyrMetAlaAsnLeuAlaLeuAlaAspLeuLeuSe

TGTCATCTGGTTCCCCTTGAAGATTGCCTATCACATACATGGCAACAACTGGATTTATGG     480
rValIleTrpPheProLeuLysIleAlaTyrHisIleHisGlyAsnAsnTrpIleTyrGl

GGAAGCTCTTTGTAATGTGCTTATTGGCTTTTTCTATCGCAACATGTACTGTTCCATTCT
yGluAlaLeuCysAsnValLeuIleGlyPhePheTyrGlyAsnMetTyrCysSerIleLu

CTTCATGACCTGCCTCAGTGTGCAGAGGTATTGGGTCATCGTGAACCCCATGGGGCACTC     600
uPheMetThrCysLeuSerValGlnArgTyrTrpValIleValAsnProMetGlyHisSe

CAGGAAGAAGGCAAACATTGCCATTGGCATCTCCCTGGCAATATGGCTGCTGACTCTGCT
rArgLysLysAlaAsnIleAlaIleGlyIleSerLeuAlaIleTrpLeuLeuThrLeuLe

GGTCACCATCCCTTTGTATGTCGTGAAGCAGACCATCTTCATTCCTGCCCTGAACATCAC     720
uValThrIleProLeuTyrValValLysGlnThrIlePheIleProAlaLeuAsnIleTh
```

FIG.11A

```
GACCTGTCATGATGTTTTGCCTGAGCAGCTCTTGGTGGGAGACATGTTCAATTACTTCCT
rThrCysHisAspValLeuProGluGlnLeuLeuValGlyAspMetPheAsnTyrPheLe

CTCTCTGGCCATTGGGGTCTTTCTGTTCCCAGCCTTCCTCACAGCCTCTGCCTATGTGCT   840
uSerLeuAlaIleGlyValPheLeuPheProAlaPheLeuThrAlaSerAlaTyrValLe

GATGATCAGAATGCTGCGATCTTCTGCCATGGATGAAAACTCAGAGAAGAAAAGGAAGAG
uMetIleArgMetLeuArgSerSerAlaMetAspGluAsnSerGluLysLysArgLysAr

GGCCATCAAACTCATTGTCACTGTCCTGGGCATGTACCTGATCTGCTTCACTCCTAGTAA   960
gAlaIleLysLeuIleValThrValLeuGlyMetTyrLeuIleCysPheThrProSerAs

CCTTCTGCTTGTGGTGCATTATTTTCTGATTAAGAGCCAGGGCCAGAGCCATGTCTATGC
nLeuLeuLeuValValHisTyrPheLeuIleLysSerGlnGlyGlnSerHisValTyrAl

CCTGTACATTGTAGCCCTCTGCCTCTCTACCCTTAACAGCTGCATCGACCCCTTTGTCTA   1080
aLeuTyrIleValAlaLeuCysLeuSerThrLeuAsnSerCysIleAspProPheValTy

TTACTTTGTTTCACATGATTTCAGGGATCATGCAAAGAACGCTCTCCTTTGCCGAAGTGT
rTyrPheValSerHisAspPheArgAspHisAlaLysAsnAlaLeuLeuCysArgSerVa

CCGCACTGTAAAGCAGATGCAAGTACCCCTCACCTCAAAGAAACACTCCAGGAAATCCAG   1200
lArgThrValLysGlnMetGlnValProLeuThrSerLysLysHisSerArgLysSerSe

CTCTTACTCTTCAAGTTCAACCACTGTTAAGACCTCCTATTGAGTTTTCCAGGTCCTCAG
rSerTyrSerSerSerSerThrThrValLysThrSerTyr

ATGGGAATTGCACAGTAGGATGTGGAACCTGTTTAATGTTATGAGGACGTGTCTGTTATT   1320

TCCGGATCCAGATCTTATTAAAGCAGAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

AAAGCAATAGCATCACAAATTTCACAAATAAAGC                             1414
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FIG. 11B

FIG. 12

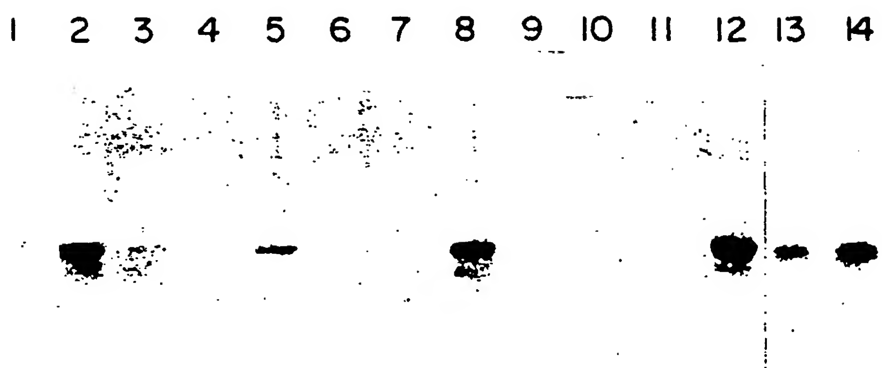

FIG. 13